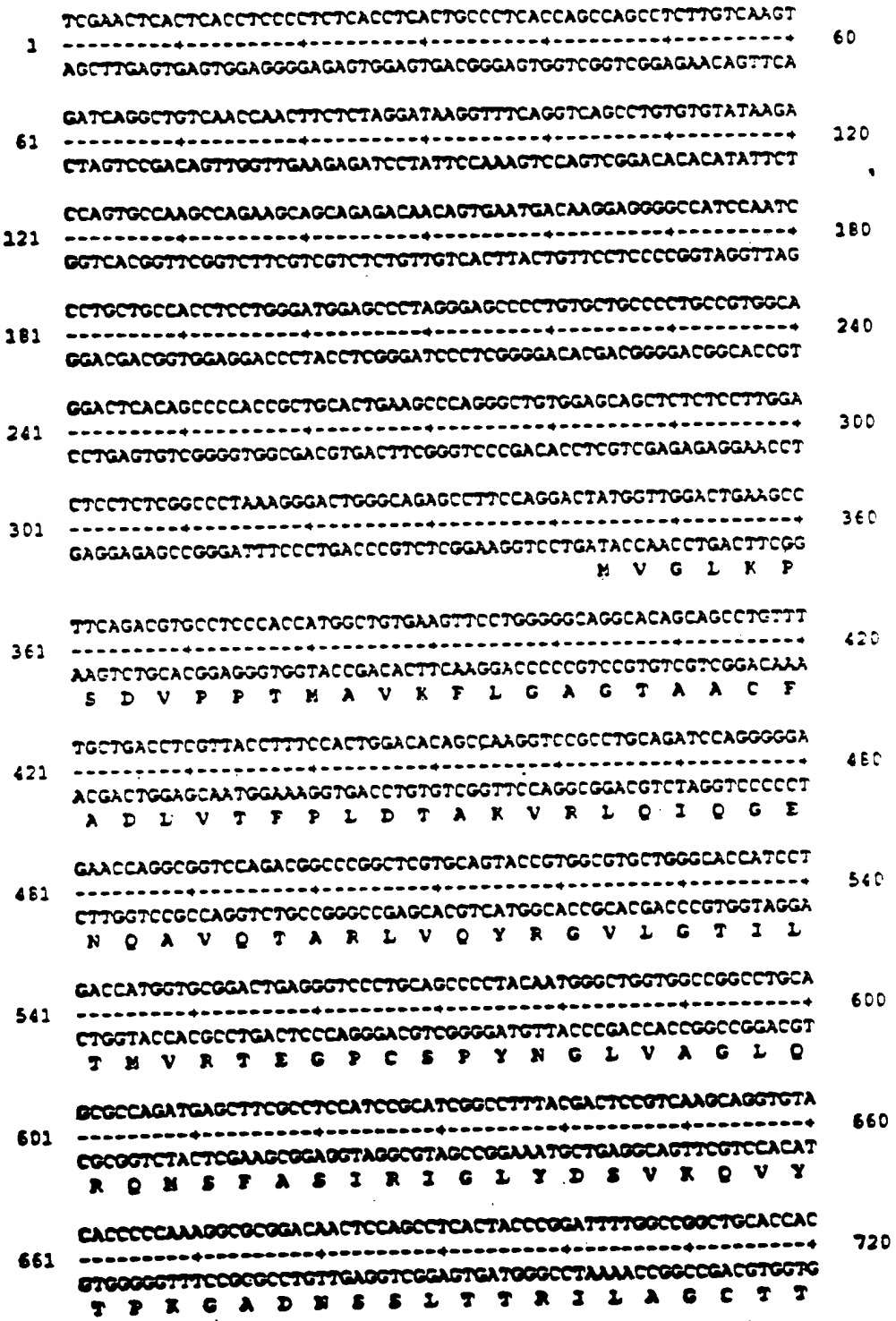
Figure 1A

1 TCGAACTCAC TCACCTCCCC TCTCACCTCA CTGCCCTCAC CAGCCAGCCT
51 CTTGTCAAGT GATCAGGCTG TCAACCAACT TCTCTAGGAT AAGGTTTCAG
101 GTCAGCCTGT GTGTATAAGA CCAGTGCCAA GCCAGAAGCA GCAGAGACAA
151 CAGTGAATGA CAAGGAGGGG CCATCCAATC CCTGCTGCCA CCTCCTGGGA
201 TGGAGCCCTA GGGAGCCCCT GTGCTGCCCC TGCCGTGGCA GGACTCACAG
251 CCCCACCGCT GCACTGAAGC CCAGGGCTGT GGAGCAGCTC TCTCCTTGGA
301 CTCCTCTCGG CCCTAAAGGG ACTGGGCAGA GCCTTCCAGG ACTATGGTTG
351 GACTGAAGCC TTCAGACGTG CCTCCCACCA TGGCTGTGAA GTTCCTGGGG
401 GCAGGCACAG CAGCCTGTTT TGCTGACCTC GTTACCTTTC CACTGGACAC
451 AGCCAAGGTC CGCCTGCAGA TCCAGGGGGA GAACCAGGCG GTCCAGACGG
501 CCCGGCTCGT GCAGTACCGT GGCGTGCTGG GCACCATCCT GACCATGGTG
551 CGGACTGAGG GTCCCTGCAG CCCCTACAAT GGGCTGGTGG CCGGCCTGCA
601 GCGCCAGATG AGCTTCGCCT CCATCCGCAT CGGCCTTTAC GACTCCGTCA
651 AGCAGGTGTA CACCCCCAAA GGCGCGGACA ACTCCAGCCT CACTACCCGG
701 ATTTTGGCCG GCTGCACCAC AGGAGCCATG GCGGTGACCT GTGCCCAGCC
751 CACAGATGTG GTGAAGGTCC GATTTCAGGC CAGCATACAC CTCGGGCCAT
801 CCAGGAGCGA CAGAAAATAC AGCGGGACTA TGGACGCCTA CAGAACCATC
851 GCCAGGGAGG AAGGAGTCAG GGGCCTGTGG AAAGGAACTT TGCCCAACAT
901 CATGAGGAAT GCTATCGTCA ACTGTGCTGA GGTGGTGACC TACGACATCC
951 TCAAGGAGAA GCTGCTGGAC TATCACCTGC TCACTGACAA CTTCCCCTGC
1001 CACTTTGTCT CTGCCTTTGG AGCCGGCTTC TGTGCCACAG TGGTGGCCTC
1051 CCCGGTGGAC GTGGTGAAGA CCCGGTATAT GAACTCACCT CCAGGCCAGT
1101 ACTTCAGCCC CCTCGACTGT ATGATAAAGA TGGTGGCCCA GGAGGGCCCC
1151 ACAGCCTTCT ACAAGGGATT TACACCCTCC TTTTTGCGTT TGGGATCCTG
1201 GAACGTGGTG ATGTTCGTAA CCTATGAGCA GCTGAAACGG GCCCTGATGA
1251 AAGTCCAGAT GTTACGGGAA TCACCGTTTT GAACAAGACA AGAAGGCCAC
1301 TGGTAGCTAA CGTGTCCGAA ACCAGTTAAG AATGGAAGAA AACGGTGCAT

Figure 1B

1351 CCACGCACAC ATGGACACAG ACCCACACAT GTTTACAGAA CTGTTGTTTA
1401 CTTGTTGCTG ATTCAAGAAA CAGAAGTAGA AGAGAGAGGA TTCTGGTCTT
1451 CACTGCCATG CCTCAAGAAC ACCTTTGTTT TGCACTGACA AGATGGAAAA
1501 TAAATTATAT TAATTTTTGA AACCCATTAG GCATGCCTAA TATTTAGGCA
1551 AGAGAAAATA AACCAAGATA GATCCATTTG GACAAAATGG AAGGTTGGAG
1601 ACGTGTATCC CCGTGAAATC TGGTCAGATA ATGAATGATA AGCAGGAAGG
1651 ATGGCAAGCA CGGGACAGGA GGGGCCCACA ATGGAGTGGG AGATCAGCCA
1701 CGGAGCCTGG AGGGACGCCA CCCAGCAACA CAGAGCTGGC GACTGCAGCT
1751 GCACCATCAC ACATGCATCA TCAGCCTATT TGTAATATGT CTGCCACAGA
1801 GAGTCCTTTG GGATTCTAGG AAACCCAAGG AACAAGAGAA AAAACTAGAG
1851 CCTGTGCTAA AGAAGCCTGC TGGGCCCATG TGAGGCTGGG GTCGTAAATA
1901 TTCCCCGACG ACACTGAAGA ATCAAGAGGG CAGCCCCCAC TTCTCCTACA
1951 AAATGGAGGG AGCCATCCCT TCCCTGTCCA CCTCACCAGG GGTGCTATGA
2001 CATGCAAGTG AGAAGCTGGG CATGAACGCA CTTTATAAAA GCAAAAGCTC
2051 TGTGTAAATC TAACTACAAG GACAATGCCT TGGGAGAGAT TTTGTCGGGA
2101 CAGAGAGGAG TTGCCAGGGA AGAAGGTTTG AAAGATACGG TTGTCTAGAG
2151 GTGAGACCAA AGGATCCAGA GACTTGGGGA CCAGAGGTGA CAGTGGATGA
2201 CGTGAAGCCA CAGGAGCCCC ACCCCCATGC AGCTTTTTCC CCACCCCCCC
2251 CACCACGCGC TCAATCATGA GTACCTCAAA GGATTGTTGG GCTTGGGGGA
2301 AAAGAGGTGG ATTCCTGGGC AAGAACCTAA AGTAGCAGGA (SEQ ID NO:11)

Figure 2A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CTAGTCCGACAGTTGGTTGAAGAGATCCTATTCCAAAGTCCAGTCGGACACACATATTCT
CCAGTGCCAAGCCAGAAGCAGCAGAGACAACAGTGAATGACAAGGAGGGGCCATCCAATC
GGTCACGGTTCGGTCTTCGTCGTCTCTGTTGTCACTTACTGTTCCTCCCCGGTAGGTTAG
CCTGCTGCCACCTCCTGGGATGGAGCCCTAGGGAGCCCCTGTGCTGCCCCTGCCGTGGCA
GGACGACGGTGGAGGACCCTACCTCGGGATCCCTCGGGGACACGACGGGGACGGCACCGT
GGACTCACAGCCCCACCGCTGCACTGAAGCCCAGGGCTGTGGAGCAGCTCTCTCCTTGGA
CCTGAGTGTCGGGGTGGCGACGTGACTTCGGGTCCCGACACCTCGTCGAGAGAGGAACCT
CTCCTCTCGGCCCTAAAGGGACTGGGCAGAGCCTTCCAGGACTATGGTTGGACTGAAGCC
GAGGAGAGCCGGGATTTCCCTGACCCGTCTCGGAAGGTCCTGATACCAACCTGACTTCGG
M V G L K P
TTCAGACGTGCCTCCCACCATGGCTGTGAAGTTCCTGGGGGCAGGCACAGCAGCCTGTTT
AAGTCTGCACGGAGGGTGGTACCGACACTTCAAGGACCCCCGTCCGTGTCGTCGGACAAA
S D V P P T M A V K F L G A G T A A C F
TGCTGACCTCGTTACCTTTCCACTGGACACAGCCAAGGTCCGCCTGCAGATCCAGGGGGA
ACGACTGGAGCAATGGAAAGGTGACCTGTGTCGGTTCCAGGCGGACGTCTAGGTCCCCCT
A D L V T F P L D T A K V R L Q I Q G E
GAACCAGGCGGTCCAGACGGCCCGGCTCGTGCAGTACCGTGGCGTGCTGGGCACCATCCT
CTTGGTCCGCCAGGTCTGCCGGGCCGAGCACGTCATGGCACCGCACGACCCGTGGTAGGA
N Q A V Q T A R L V Q Y R G V L G T I L
GACCATGGTGCGGACTGAGGGTCCCTGCAGCCCCTACAATGGGCTGGTGGCCGGCCTGCA
CTGGTACCACGCCTGACTCCCAGGGACGTCGGGGATGTTACCCGACCACCGGCCGGACGT
T M V R T E G P C S P Y N G L V A G L Q
GCGCCAGATGAGCTTCGCCTCCATCCGCATCGGCCTTTACGACTCCGTCAAGCAGGTGTA
CGCGGTCTACTCGAAGCGGAGGTAGGCGTAGCCGGAAATGCTGAGGCAGTTCGTCCACAT
R Q M S F A S I R I G L Y D S V K Q V Y
CACCCCCAAAGGCGCGGACAACTCCAGCCTCACTACCCGGATTTTGGCCGGCTGCACCAC
GTGGGGGTTTCCGCGCCTGTTGAGGTCGGAGTGATGGGCCTAAAACCGGCCGACGTGGTG
T P K G A D N S S L T T R I L A G C T T

Figure 2B

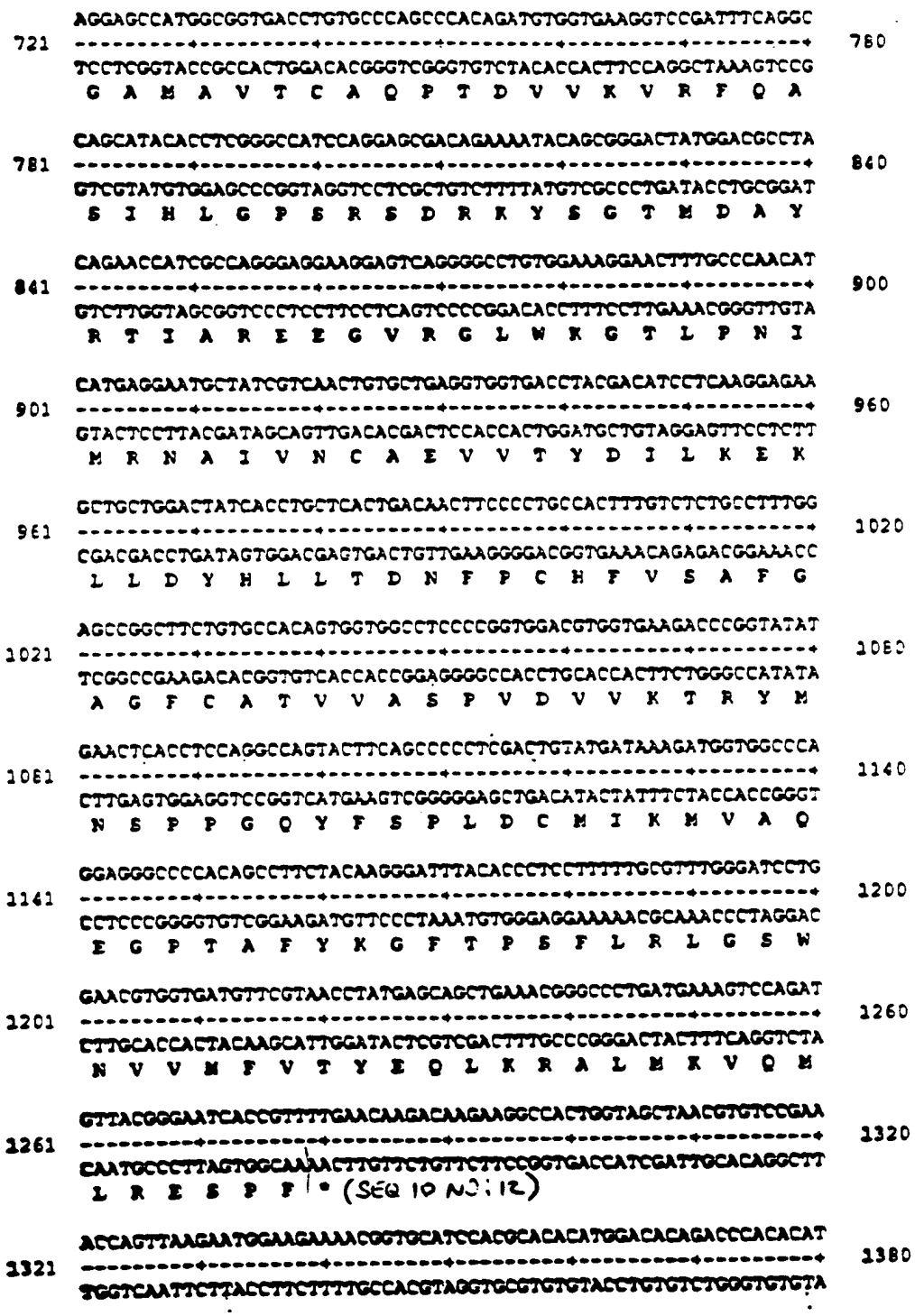


Figure 2C

```
                GTTTACAGAACTGTTGTTTACTTGTTGCTGATTCAAGAAACAGAAGTAGAAGAGAGAGGA
1381            ---------+---------+---------+---------+---------+---------+  1440
                CAAATGTCTTGACAACAAATGAACAACGACTAAGTTCTTTGTCTTCATCTTCTCTCTCCT

                TTCTGGTCTTCACTGCCATGCCTCAAGAACACCTTTGTTTTGCACTGACAAGATGGAAAA
1441            ---------+---------+---------+---------+---------+---------+  1500
                AAGACCAGAAGTGACGGTACGGAGTTCTTGTGGAAACAAAACGTGACTGTTCTACCTTTT

                TAAATTATATTAATTTTTGAAACCCATTAGGCATGCCTAATATTTAGGCAAGAGAAAATA
1501            ---------+---------+---------+---------+---------+---------+  1560
                ATTTAATATAATTAAAAACTTTGGGTAATCCGTACGGATTATAAATCCGTTCTCTTTTAT

                AACCAAGATAGATCCATTTGGACAAAATGGAAGGTTGGAGACGTGTATCCCCGTGAAATC
1561            ---------+---------+---------+---------+---------+---------+  1620
                TTGGTTCTATCTAGGTAAACCTGTTTTACCTTCCAACCTCTGCACATAGGGGCACTTTAG

                TGGTCAGATAATGAATGATAAGCAGGAAGGATGGCAAGCACGGGACAGGAGGGGCCCACA
1621            ---------+---------+---------+---------+---------+---------+  1680
                ACCAGTCTATTACTTACTATTCGTCCTTCCTACCGTTCGTGCCCTGTCCTCCCCGGGTGT

                ATGGAGTGGGAGATCAGCCACGGAGCCTGGAGGGACGCCACCCAGCAACACAGAGCTGGC
1681            ---------+---------+---------+---------+---------+---------+  1740
                TACCTCACCCTCTAGTCGGTGCCTCGGACCTCCCTGCGGTGGGTCGTTGTGTCTCGACCG

                GACTGCAGCTGCACCATCACACATGCATCATCAGCCTATTTGTAATATGTCTGCCACAGA
1741            ---------+---------+---------+---------+---------+---------+  1800
                CTGACGTCGACGTGGTAGTGTGTACGTAGTAGTCGGATAAACATTATACAGACGGTGTCT

                GAGTCCTTTGGGATTCTAGGAAACCCAAGGAACAAGAGAAAAAACTAGAGCCTGTGCTAA
1801            ---------+---------+---------+---------+---------+---------+  1860
                CTCAGGAAACCCTAAGATCCTTTGGGTTCCTTGTTCTCTTTTTTGATCTCGGACACGATT

                AGAAGCCTGCTGGGCCCATGTGAGGCTGGGGTCGTAAATATTCCCCGACGACACTGAAGA
1861            ---------+---------+---------+---------+---------+---------+  1920
                TCTTCGGACGACCCGGGTACACTCCGACCCCAGCATTTATAAGGGGCTGCTGTGACTTCT

                ATCAAGAGGGCAGCCCCCACTTCTCCTACAAAATGGAGGGAGCCATCCCTTCCCTGTCCA
1921            ---------+---------+---------+---------+---------+---------+  1980
                TAGTTCTCCCGTCGGGGGTGAAGAGGATGTTTTACCTCCCTCGGTAGGGAAGGGACAGGT

                CCTCACCAGGGGTGCTATGACATGCAAGTGAGAAGCTGGGCATGAACGCACTTTATAAAA
1981            ---------+---------+---------+---------+---------+---------+  2040
                GGAGTGGTCCCCACGATACTGTACGTTCACTCTTCGACCCGTACTTGCGTGAAATATTTT

                GCAAAAGCTCTGTGTAAATCTAACTACAAGGACAATGCCTTGGGAGAGATTTTGTCGGGA
2041            ---------+---------+---------+---------+---------+---------+  2100
                CGTTTTCGAGACACATTTAGATTGATGTTCCTGTTACGGAACCCTCTCTAAAACAGCCCT

                CAGAGAGGAGTTGCCAGGGAAGAAGGTTTGAAAGATACGGTTGTCTAGAGGTGAGACCAA
2101            ---------+---------+---------+---------+---------+---------+  2160
                GTCTCTCCTCAACGGTCCCTTCTTCCAAACTTTCTATGCCAACAGATCTCCACTCTGGTT

                AGGATCCAGAGACTTGGGGACCAGAGGTGACAGTGGATGACGTGAAGCCACAGGAGCCCC
```

Figure 2D

```
2161 ---------+---------+---------+---------+---------+---------+ 2220
     TCCTAGGTCTCTGAACCCCTGGTCTCCACTGTCACCTACTGCACTTCGGTGTCCTCGGGG

     ACCCCCATGCAGCTTTTTTCCCCACCCCCCCACCACGCGCTCAATCATGAGTACCTCAAA
2221 ---------+---------+---------+---------+---------+---------+ 2280
     TGGGGGTACGTCGAAAAAAGGGGTGGGGGGGTGGTGCGCGAGTTAGTACTCATGGAGTTT

     GGATTGTTGGGCTTGGGGGAAAAGAGGTGGATTCCTGGGCAAGAACCTAAAGTAGCAGGA
2281 ---------+---------+---------+---------+---------+---------+ 2340
     CCTAACAACCCGAACCCCCTTTTCTCCACCTAAGGACCCGTTCTTGGATTTCATCGTCCT
```

Figure 3

```
  1  MVGLKPSDVP PTMAVKFLGA GTAACFADLV TFPLDTAKVR LQIQGENQAV
 51  QTARLVQYRG VLGTILTMVR TEGPCSPYNG LVAGLQRQMS FASIRIGLYD
101  SVKQVYTPKG ADNSSLTTRI LAGCTTGAMA VTCAQPTDVV KVRFQASIHL
151  GPSRSDRKYS GTMDAYRTIA REEGVRGLWK GTLPNIMRNA IVNCAEVVTY
201  DILKEKLLDY HLLTDNFPCH FVSAFGAGFC ATVVASPVDV VKTRYMNSPP
251  GQYFSPLDCM IKMVAQEGPT AFYKGFTPSF LRLGSWNVVM FVTYEQLKRA
301  LMKVQMLRES PF*  (SEQ ID NO:12)
```

Northern Aanlysis of UCP3 Expression in Human Tissues

Figure 4

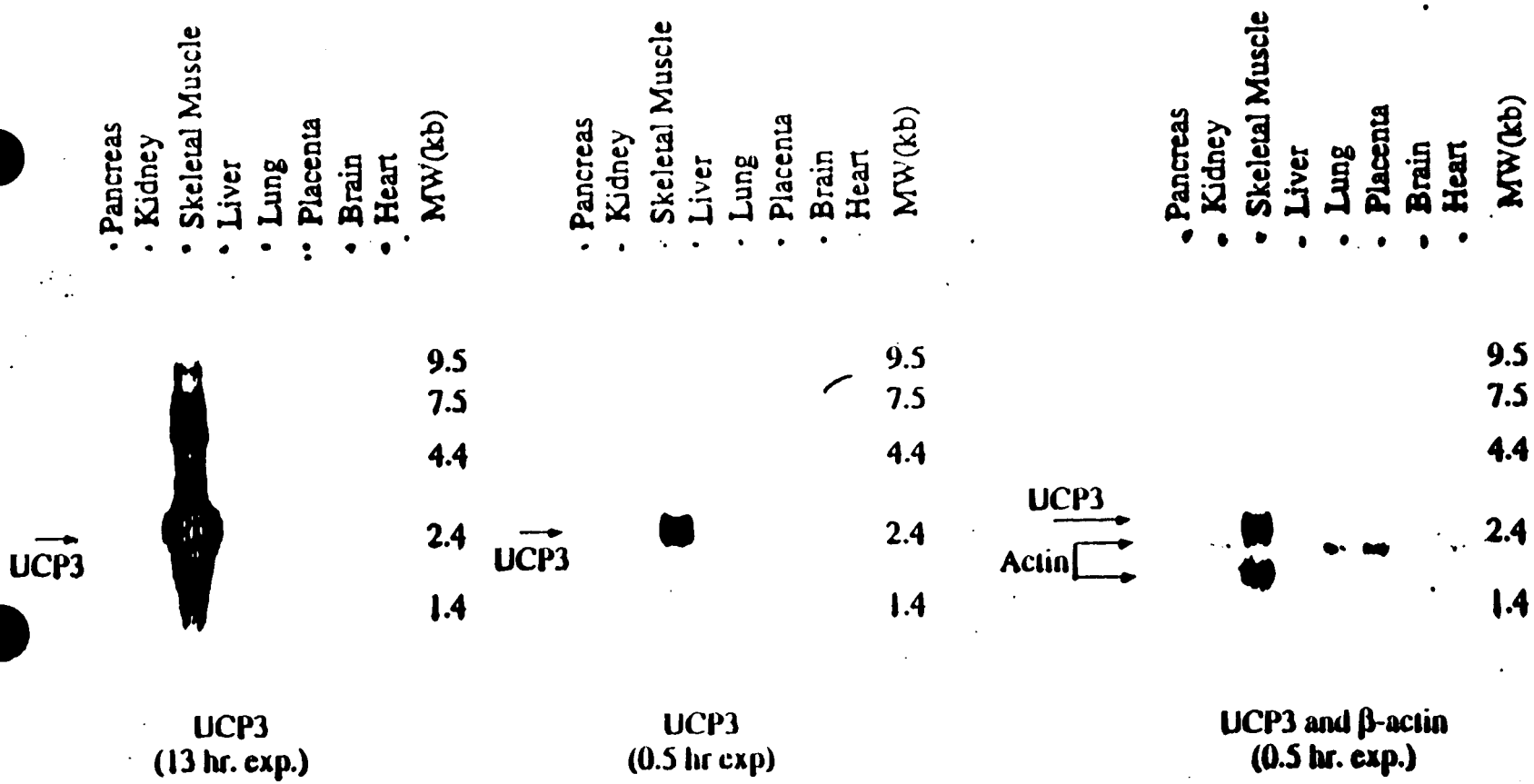
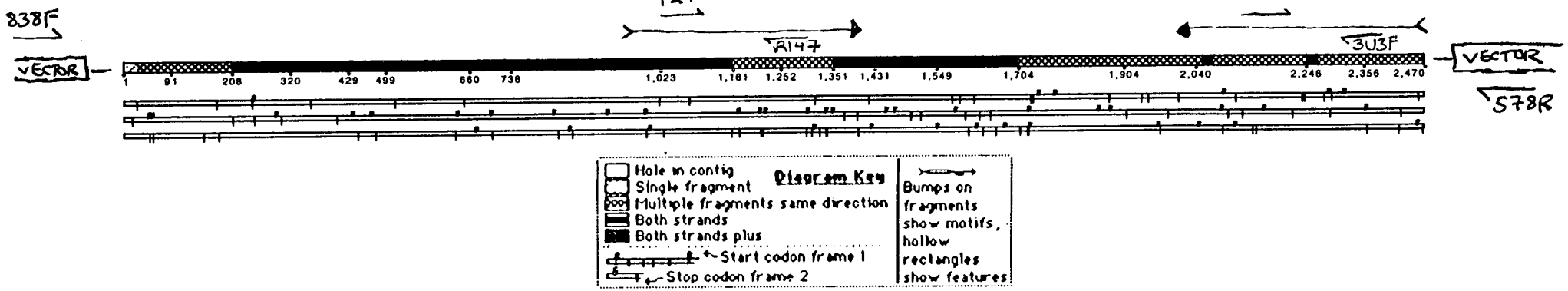


FIGURE 5

5'EST
AA192136

3'EST
AA192553



```
   1  CCAGGAACAG CAGAGACAAC AGTGAATGGT GAGGCCCGGC CGTCAGATCC
  51  TGCTGCTACC TAATGGAGTG GATCCTTAGG GTGGCCCTGC ACTACCCAAC
 101  CTTGGCTAGA CGCACAGCTT CCTCCCTGAA CTGAAGCAAA AGATTGCCAG
 151  GCAAGCTCTC TCCTCGGACC TCCATAGGCA GCAAAGGAAC CAGGCCCATT
 201  CCCCGGGACC ATGGTTGGAC TTCAGCCCTC CGAAGTGCCT CCCACAACGG
 251  TTGTGAAGTT CCTGGGGGCC GGCACTGCGG CCTGTTTTGC GGACCTCCTC
 301  ACTTTTCCCC TGGACACCGC CAAGGTCCGT CTGCAGATCC AAGGGGAGAA
 351  CCCAGGGGCT CAGAGCGTGC AGTACCGCGG TGTGCTGGGT ACCATCCTGA
 401  CTATGGTGCG CACAGAGGGT CCCCGCAGCC CCTACAGCGG ACTGGTCGCT
 451  GGCCTGCACC GCCAGATGAG TTTTGCCTCC ATTCGAATTG GCCTCTACGA
 501  CTCTGTCAAG CAGTTCTACA CCCCCAAGGG AGCGGACCAC TCCAGCGTCG
 551  CCATCAGGAT TCTGGCAGGC TGCACGACAG GAGCCATGGC AGTGACCTGC
 601  GCCCAGCCCA CGGATGTGGT GAAGGTCCGA TTTCAAGCCA TGATACGCCT
 651  GGGAACTGGA GGAGAGAGGA AATACAGAGG GACTATGGAT GCCTACAGAA
 701  CCATCGCCAG GGAGGAAGGA GTCAGGGGCC TGTGGAAAGG GACTTGGCCC
 751  AACATCACAA GAAATGCCAT TGTCAACTGT GCTGAGATGG TGACCTACGA
 801  CATCATCAAG GAGAAGTTGC TGGAGTCTCA CCTGTTTACT GACAACTTCC
 851  CCTGTCACTT TGTCTCTGCC TTTGGAGCTG GCTTCTGTGC CACAGTGGTG
 901  GCCTCCCCGG TGGATGTGGT AAAGACCCGA TACATGAACG CTCCCCTAGG
 951  CAGGTACCGC AGCCCTCTGC ACTGTATGCT GAAGATGGTG GCTCAGGAGG
```

FIGURE 6A

```
1001  GACCCACGGC CTTCTACAAA GGATTTGTGC CCTCCTTTCT GCGTCTGGGA
1051  GCTTGGAACG TGATGATGTT TGTAACATAT GAGCAACTGA AGAGGGCCTT
1101  AATGAAAGTC CAGGTACTGC GGGAATCTCC GTTTTGAACA AGGCAAGCAG
1151  GCTGCCTGGA ACAGAACAAA GCGTCTCTGC CCTGGGGACA CAGGCCCACA
1201  CGGTCCAGAA CCCTGCACTG CTGCTGACAC GAGAAACTGA ACTAAAAGAG
1251  GAGAGTTTTA GTCCTCCGTG TTTCGTCCTA AAACACCTCT GTTTTGCACT
1301  GACCTGATGG GAAATAAATT ATATTAATTT TTAAACCCTT TCCGGTTGGA
1351  TGCCTAACAT TTAGGCAAGA GACAACAAAG AAAACCAGAG TCAACTCCCT
1401  TGAAATGTAG GAATAAAGGA TGCATAATAA ACAGGAAAGG CACAGGTTTT
1451  GAGAAGATCA GCCCACAGTG TTGTCCTTGA ATCAAACAAA ATGGTCGGAG
1501  GAACCCTTCG GGTTCAGCAC AAAGAGGTGA CTACAGCCTT TTGGTCACCA
1551  GATGACTCCG CCCCTTTGTA ATGAGTCTGC CAAGTAGACT CTATCAAGAT
1601  TCTGGGGAAA GGAGAAAGAA CACATTGACC TGCCCGGGCG GCCGCTCGAG
1651  CCCTATGA (SEQ ID NO:17)
```

FIGURE 6B

```
  1  MVGLQPSEVP PTTVVKFLGA GTAACFADLL TFPLDTAKVR LQIQGENPGA
 51  QSVQYRGVLG TILTMVRTEG PRSPYSGLVA GLHRQMSFAS IRIGLYDSVK
101  QFYTPKGADH SSVAIRILAG CTTGAMAVTC AQPTDVVKVR FQAMIRLGTG
151  GERKYRGTMD AYRTIAREEG VRGLWKGTWP NITRNAIVNC AEMVTYDIIK
201  EKLLESHLFT DNFPCHFVSA FGAGFCATVV ASPVDVVKTR YMNAPLGRYR
251  SPLHCMLKMV AQEGPTAFYK GFVPSFLRLG AWNVMMFVTY EQLKRALMKV
301  QVLRESPF* (SEQ ID NO:18)
```


FIGURE 7

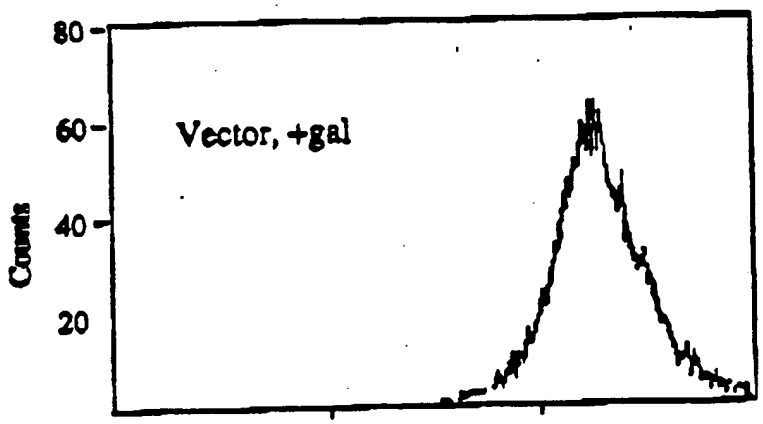


FIGURE 8A

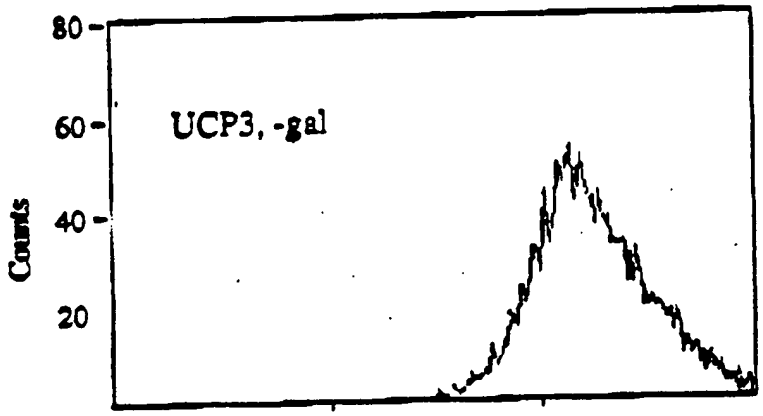


FIGURE 8B

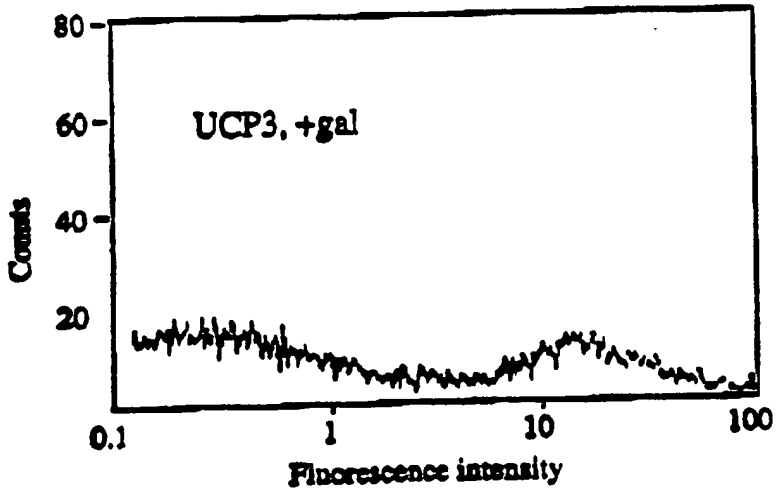


FIGURE 8C

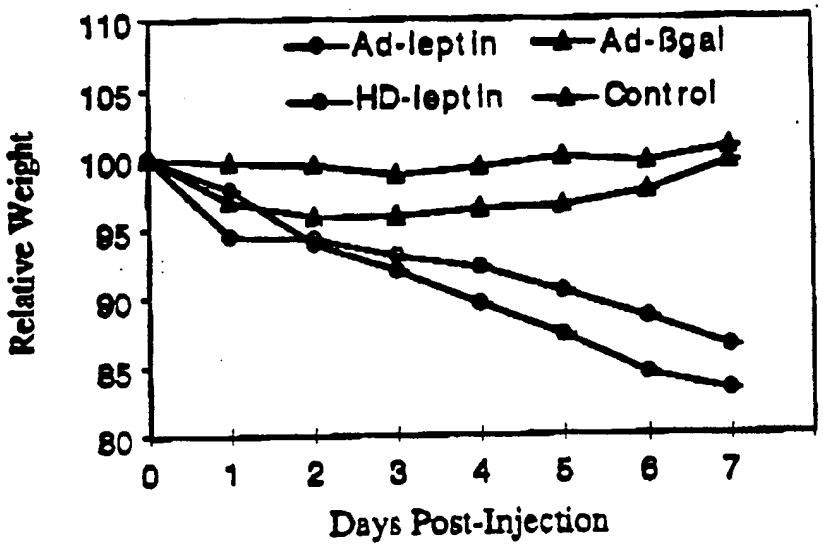


FIGURE 9A

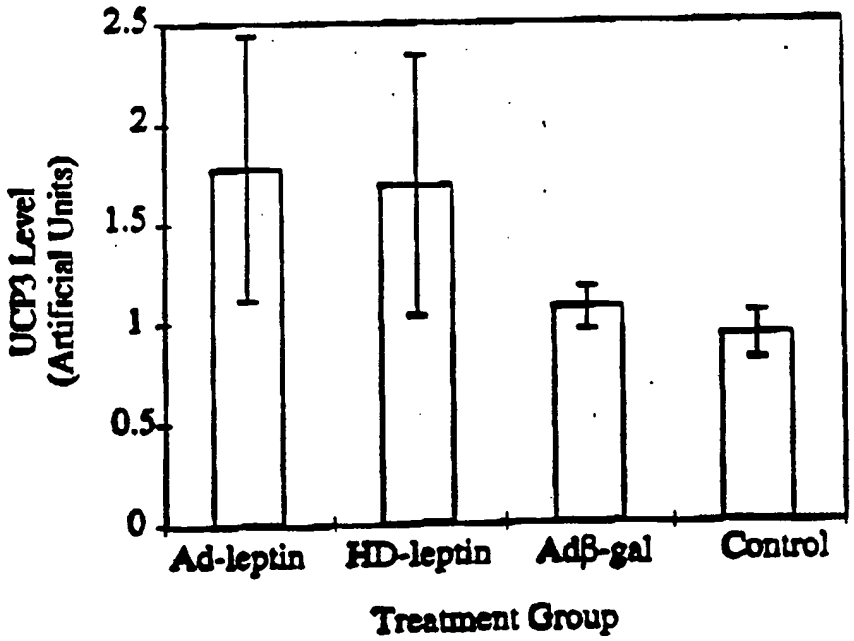


FIGURE 9B